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Integrated Pest Management

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On the potential of population genetics to refine scales for locust management

Marie-Pierre Chapuis¹, Karine Berthier², Julie-Anne Popple³, Gregory Sword⁴

¹CIRAD, France, ²INRA, France, ³University of Sydney, Australia, ⁴Texas A&M University, United States Minor Outlying Islands

Linking demographic and genetic dispersal measures is of fundamental importance for movement ecology and evolution. However, such integration can be difficult, particularly for highly fecund species that are often the target of management decisions guided by an understanding of population movement. Here, we present an example of how the influence of large population sizes can preclude genetic approaches from assessing demographic population structuring, even at a continental scale. The Australian plague locust, *Chortoicetes terminifera*, is a significant pest, with populations on the eastern and western sides of Australia having been monitored and managed independently to date. We used microsatellites to assess genetic variation in 12 *C. terminifera* population samples separated by up to 3000 km. Traditional summary statistics indicated high levels of genetic diversity and a surprising lack of population structure across the entire range. An approximate Bayesian computation treatment indicated that levels of genetic diversity in *C. terminifera* corresponded to effective population sizes conservatively composed of tens of thousands to several million individuals. We used these estimates and computer simulations to estimate the minimum rate of dispersal that could account for the observed range-wide genetic homogeneity. The rate of dispersal between both sides of the Australian continent could be several orders of

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